

## SEQUENCE LISTING

<110> SES EUROPE N.V./S.A.

<120> METHOD OF GENETIC MODIFICATION OF A WILD TYPE VIRAL  
SEQUENCE

<130> P.SES.02/WO

<140>

<141>

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(399)

<220>

<223> Description of Artificial Sequence: genetically  
modified TGB-3 viral sequence

<400> 1

atg	gtg	ctt	gtg	ggt	gca	gta	gct	tta	tct	aat	att	gta	ttg	tac	ata	48
Met	Val	Leu	Val	Val	Ala	Val	Ala	Leu	Ser	Asn	Ile	Val	Leu	Tyr	Ile	
1				5				10					15			

ggt	gcc	ggt	tgt	ggt	ggt	gtc	agt	atg	ttg	tac	tca	ccg	ttt	ttc	agc	96
Val	Ala	Gly	Cys	Val	Val	Val	Ser	Met	Leu	Tyr	Ser	Pro	Phe	Phe	Ser	
			20				25					30				

aac	gat	ggt	aaa	gcg	tcc	agc	tat	gcg	gga	gca	att	ttt	aag	ggg	agc	144
Asn	Asp	Val	Lys	Ala	Ser	Ser	Tyr	Ala	Gly	Ala	Ile	Phe	Lys	Gly	Ser	
		35					40					45				

ggc	tgt	atc	atg	gac	agg	aat	tgc	ttt	gct	caa	ttt	ggg	agt	tgc	gat	192
Gly	Cys	Ile	Met	Asp	Arg	Asn	Ser	Phe	Ala	Gln	Phe	Gly	Ser	Cys	Asp	
	50					55					60					

att	cca	aag	cat	gta	gcc	gag	tcc	atc	act	aag	ggt	gcc	acc	aaa	gag	240
Ile	Pro	Lys	His	Val	Ala	Glu	Ser	Ile	Thr	Lys	Val	Ala	Thr	Lys	Glu	

65	70	75	80
cac gat gtt gac ata atg gta aaa agg ggt gaa gtg acc gtt cgt gtt			288
His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val			
	85	90	95
gtg act ctc acc gaa act att ttt ata ata tta tct aga ttg ttt ggt			336
Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly			
	100	105	110
ttg gcg gtg ttt ttg ttc atg ata tgt tta atg tct ata gtt tgg ttt			384
Leu Ala Val Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe			
	115	120	125
tggtatcatagataa			399
Trp Tyr His Arg			
130			

&lt;210&gt; 2

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: genetically  
modified TGB-3 viral sequence

&lt;400&gt; 2

Met Val Leu Val Val Ala Val Ala Leu Ser Asn Ile Val Leu Tyr Ile			
1	5	10	15
Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser			
	20	25	30
Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser			
	35	40	45
Gly Cys Ile Met Asp Arg Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp			
	50	55	60
Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu			
65	70	75	80
His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val			
	85	90	95
Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly			
	100	105	110

Leu Ala Val Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe  
 115 120 125

Trp Tyr His Arg  
 130

<210> 3

<211> 399

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(399)

<220>

<223> Description of Artificial Sequence: genetically  
 modified TGB-3 viral sequence

<400> 3

atg gtg ctt gtg gtt aaa gta gat tta tct aat att gta ttg tac ata	48
Met Val Leu Val Val Lys Val Asp Leu Ser Asn Ile Val Leu Tyr Ile	
1 5 10 15	
ggt gcc ggt tgt gtt gtt gtc agt atg ttg tac tca ccg ttt ttc agc	96
Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser	
20 25 30	
aac gat gtt aaa gcg tcc agc tat gcg gga gca att ttt aag ggg agc	144
Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser	
35 40 45	
ggc tgt atc atg gcc gcg aat tcg ttt gct caa ttt ggg agt tgc gat	192
Gly Cys Ile Met Ala Ala Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp	
50 55 60	
att cca aag cat gta gcc gag tcc atc act aag gtt gcc acc aaa gag	240
Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu	
65 70 75 80	
cac gat gtt gac ata atg gta aaa agg ggt gaa gtg acc gtt cgt gtt	288
His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val	
85 90 95	
gtg act ctc acc gaa act att ttt ata ata tta tct aga ttg ttt ggt	336
Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly	

100

105

110

ttg gcg gtg ttt ttg ttc atg ata tgt tta atg tct ata gtt tgg ttt 384  
 Leu Ala Val Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe

115

120

125

tgg tat cat aga taa

399

Trp Tyr His Arg

130

&lt;210&gt; 4

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: genetically  
 modified TGB-3 viral sequence

&lt;400&gt; 4

Met Val Leu Val Val Lys Val Asp Leu Ser Asn Ile Val Leu Tyr Ile  
 1 5 10 15

Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser  
 20 25 30

Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser  
 35 40 45

Gly Cys Ile Met Ala Ala Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp  
 50 55 60

Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu  
 65 70 75 80

His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val  
 85 90 95

Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly  
 100 105 110

Leu Ala Val Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe  
 115 120 125

Trp Tyr His Arg

130

&lt;210&gt; 5

&lt;211&gt; 399

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(399)

&lt;220&gt;

<223> Description of Artificial Sequence: genetically  
modified TGB-3 viral sequence

&lt;400&gt; 5

atg gtg ctt gtg gtt aaa gta gat tta tct aat att gta ttg tac ata	48
Met Val Leu Val Val Lys Val Asp Leu Ser Asn Ile Val Leu Tyr Ile	
1 5 10 15	
gtt gcc ggt tgt gtt gtt gtc agt atg ttg tac tca ccg ttt ttc agc	96
Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser	
20 25 30	
aac gat gtt aaa gcg tcc agc tat gcg gga gca att ttt aag ggg agc	144
Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser	
35 40 45	
ggc tgt atc atg gac agg aat tcg ttt gct caa ttt ggg agt tgc gat	192
Gly Cys Ile Met Asp Arg Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp	
50 55 60	
att cca aag cat gta gcc gag tcc atc act aag gtt gcc acc aaa gag	240
Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu	
65 70 75 80	
cac gat gtt gac ata atg gta aaa agg ggt gaa gtg acc gtt cgt gtt	288
His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val	
85 90 95	
gtg act ctc acc gaa act att ttt ata ata tta tct aga ttg ttt ggt	336
Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly	
100 105 110	
ttg gat gat ttt ttg ttc atg ata tgt tta atg tct ata gtt tgg ttt	384
Leu Asp Asp Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe	
115 120 125	
tgg tat cat aga taa	399
Trp Tyr His Arg	

130

&lt;210&gt; 6

&lt;211&gt; 132

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<223> Description of Artificial Sequence: genetically  
modified TGB-3 viral sequence

&lt;400&gt; 6

Met Val Leu Val Val Lys Val Asp Leu Ser Asn Ile Val Leu Tyr Ile  
1 5 10 15

Val Ala Gly Cys Val Val Val Ser Met Leu Tyr Ser Pro Phe Phe Ser  
20 25 30

Asn Asp Val Lys Ala Ser Ser Tyr Ala Gly Ala Ile Phe Lys Gly Ser  
35 40 45

Gly Cys Ile Met Asp Arg Asn Ser Phe Ala Gln Phe Gly Ser Cys Asp  
50 55 60

Ile Pro Lys His Val Ala Glu Ser Ile Thr Lys Val Ala Thr Lys Glu  
65 70 75 80

His Asp Val Asp Ile Met Val Lys Arg Gly Glu Val Thr Val Arg Val  
85 90 95

Val Thr Leu Thr Glu Thr Ile Phe Ile Ile Leu Ser Arg Leu Phe Gly  
100 105 110

Leu Asp Asp Phe Leu Phe Met Ile Cys Leu Met Ser Ile Val Trp Phe  
115 120 125

Trp Tyr His Arg  
130